



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jofuku, K. Diane
Okamuro, Jack K.

(ii) TITLE OF INVENTION: Methods for Improving Seeds

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/879,827
(B) FILING DATE: 20-JUN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/700,152
(B) FILING DATE: 20-AUG-1996

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr Arg Gly

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Trp Glu Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1680
- (D) OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCTCTCT	CTCTTAGCT	CTTTTTTT	TTTGTTTC	ATTAAGTTT	TTATTTATT	60
TTCTACCAAC	CAAAAGCTT	TCTCTTGGT	TTCTCTTATT	TAGCTTCTAA	CCTTGAGGAG	120
AATATACCAAG	AGGATTGAAG	TTTGAACCTT	CAAAGATCAA	AATCAAGAAA	CCAAAAAA	180
ACAAAAAA	TGTGGGATCT	AAACGACGCA	CCACACCAA	CACAAAGAGA	AGAAGAATCT	240
GAAGAGTTT	GTTATTCTTC	ACCAAGTAAA	CGGGTTGGAT	CTTTCTCTAA	TTCAAGCTCT	300
TCAGCTGTTG	TTATCGAAGA	TGGATCCGAT	GACGATGAAC	TTAACCGGGT	CAGACCCAAT	360

AACCCACTTG	TCACCCATCA	GTTCTTCCT	GAGATGGATT	CTAACGGCGG	TGGTGGCT	420
TCTGGCTTC	CTCGGGCTCA	CTGGTTGGT	GTAAAGTTT	GTCAGTCGGA	TCTAGCCACC	480
GGATCGTCCG	CGGGTAAAGC	TACCAACGTT	GCCGCTGCCG	TAGTGGAGCC	GGCACAGCCG	540
TTGAAAAAGA	GTCGGCGTGG	ACCAAGATCA	AGAAGTTCTC	AGTATAGAGG	TGTTACGTT	600
TACCGGCGTA	CCGGAAGATG	GGAATCTCAT	ATTGGGACT	GTGGGAAACA	AGTTTACTTA	660
GGTGGATTG	ACACTGCTCA	TGCAGCAGCT	CGAGCATATG	ATAGAGCTGC	TATTAAATTC	720
CGTGGAGTAG	AAGCGGATAT	CAATTCAAC	ATCGACGATT	ATGATGATGA	CTTGAAACAG	780
ATGACTAATT	TAACCAAGGA	AGAGTCGTA	CACGTACTTC	GCCGACAAAG	CACAGGCTTC	840
CCTCGAGGAA	GTTCGAAGTA	TAGAGGTGTC	ACTTGCATA	AGTGTGGTCG	TTGGGAAGCT	900
CGTATGGGTC	AATTCTTAGG	CAAAAAGTAT	GTTCATTTGG	GTTCATTTGG	CACCGAGGTC	960
GAAGCTGCTA	GAGCTTACGA	TAAAGCTGCA	ATCAAATGTA	ACGGCAAAGA	CGCCGTGACC	1020
AACTTGATC	CGAGTATTG	CGATGAGGAA	CTCAATGCCG	AGTCATCAGG	GAATCCTACT	1080
ACTCCACAAG	ATCACAAACCT	CGATCTGAGC	TTGGGAAATT	CGGCTAATTC	GAAGCATAAA	1140
AGTCAAGATA	TGCGGCTCAG	GATGAACCAA	CAACAACAAG	ATTCTCTCCA	CTCTAATGAA	1200
GTTCTGGAT	TAGGTCAAAC	CGGAATGCTT	AACCATACTC	CCAATTCAAA	CCACCAATT	1260
CCGGGCAGCA	GCAACATTGG	TAGCGGAGGC	GGATTCTCAC	TGTTCCGGC	GGCTGAGAAC	1320
CACCGGTTTG	ATGGTCGGGC	CTCGACGAAC	CAAGTGTGA	CAAATGCTGC	AGCATCATCA	1380
GGATTCTCTC	CTCATCATCA	CAATCAGATT	TTTAATTCTA	CTTCTACTCC	TCATCAAAAT	1440
TGGCTGCAGA	CAAATGGCTT	CCAACCTCCT	CTCATGAGAC	CTTCTTGAAT	CTTTTATATT	1500
TTTAAGGTTT	ATTATTATAT	AAGAAAAACA	AAAATGAACC	TTTGAAATCC	CCACATGTT	1560
TTGGTCATT	CATTAATCAT	CGGCTTATAT	TTTGCTTATT	TTCCCTAAA	TCCTCTTGT	1620
AACTTAGGCG	AACAAAAAAA	ATTAATGGAA	ATCTTTTCC	CTCCATCGGT	TACAAAAATA	1680

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..67
 - (D) OTHER INFORMATION: /note= "AP2-R1 direct repeat at positions 129 to 195"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 32..49
- (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix (SEQ ID NO:6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15

Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
 20 25 30

Thr Asp Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
 35 40 45

Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp
 50 55 60

Asp Asp Leu
 65

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "AP2-R2 direct repeat at positions 221 to 288"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..50
- (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic alpha-helix (SEQ ID NO:7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
 1 5 10 15

Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu
 20 25 30

Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
 35 40 45

Lys Cys Asn Gly Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr
 50 55 60
 Asp Glu Glu Leu
 65

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Phe Asp Thr Ala His Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile
 1 5 10 15

Lys Phe

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
 1 5 10 15

Lys Cys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Ala Tyr Asp
1

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

*Cl
C1
Cn*

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: /note= "ANT-R1 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 44..59
- (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic alpha-helix (SEQ ID NO:37)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
1 5 10 15

Glu Ala His Leu Trp Asp Asn Ser Phe Lys Lys Glu Gly His Ser Arg
20 25 30

Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala
35 40 45

Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr
50 55 60

His Thr Asn Phe Ser Ala Glu Asn Tyr Gln Lys Glu Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "ANT-R2 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 37..51
- (D) OTHER INFORMATION: /note= "putative ANT-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
 1 5 10 15

Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
 20 25 30

Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala
 35 40 45

Ile Lys Phe Arg Gly Thr Asn Ala Val Thr Asn Phe Asp Ile Thr Arg
 50 55 60

Tyr Asp Val Asp Arg
 65

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "RAP2.7-R1 direct repeat"

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION: 33..49

(D) OTHER INFORMATION: /note= "putative RAP2.7-R1 amphipathic alpha helix (SEO ID NO:36)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15

Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
20 25 30

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Arg Ala Ala Ile Lys
35 40 45

Phe Arg Gly Val Asp Ala Asp Ile Asn Phe Thr Leu Gly Asp Tyr Glu
 50 55 60

Glu Asp Met
65

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE 'CHARACTERISTICS':

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION: 26°.34'

(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12.

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Cys Gly Arg Ile Glu
1 5 10 15

Ala Arg Met Gly Gin Phe Leu Gly Lys Lys Ala Tyr Asp Lys Ala Ala
20 25 30

11e Asn Thr Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Met Ser Ser
35 40 45

Tyr Gln Asn Glu Ile
50

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Tyr Arg Gly Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Ser"

C1
Arg
(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Arg Trp Glu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Tyr Leu Gly
1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Ala Ile Lys
1

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-1"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..51
- (D) OTHER INFORMATION: /note= "putative EREBP-1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
1 5 10 15

Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
20 25 30

Thr Tyr Glu Thr Asp Glu Glu Ala Ala Ile Ala Tyr Asp Lys Ala Ala
35 40 45

Tyr Arg Met Arg Gly Ser Lys Ala His Leu Asn Phe Pro Leu Glu Val
50 55 60

Ala Asn Phe Lys Gln
65

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..69
 - (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-2"
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION: 35..51
 - (D) OTHER INFORMATION: /note= "putative EREBP-2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
 20 25 30
 Thr Tyr Glu Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala
 35 40 45
 Tyr Arg Met Arg Gly Ser Lys Ala Leu Leu Asn Phe Pro His Arg Ile
 50 55 60
 Gly Leu Asn Glu Pro
 65

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-3"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative EREBP-3 amphipathic alpha-helix (SEQ ID NO:41)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu	Val	His	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Pro	Trp	Gly	Arg	Tyr	Ala
1					5					10				15	

Ala	Glu	Ile	Arg	Asp	Pro	Gly	Lys	Lys	Ser	Arg	Val	Trp	Leu	Gly	Thr
	20						25						30		

Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Lys	Ala	Tyr	Asp	Thr	Ala	Ala	Arg
	35						40					45			

Glu	Phe	Arg	Gly	Pro	Lys	Ala	Lys	Thr	Asn	Phe	Pro	Ser	Pro	Thr	Glu
	50				55					60					

Asn	Gln	Ser	Pro
	65		

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-4"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..51
- (D) OTHER INFORMATION: /note= "putative EREBP-4 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys	Lys	His	Tyr	Arg	Gly	Val	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Phe	Ala
1					5					10			15		

Ala Glu Ile Arg Asp Pro Asn Arg Lys Gly Thr Arg Val Trp Leu Gly
 20 25 30

Thr Phe Asp Thr Ala Ile Glu Ala Ala Lys Ala Tyr Asp Arg Ala Ala
 35 40 45

Phe Lys Leu Arg Gly Ser Lys Ala Ile Val Asn Phe Pro His Arg Ile
 50 55 60

Gly Leu Asn Glu Pro
 65

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.2 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic alpha-helix (SEQ ID NO:38)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15

Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr
 20 25 30

Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg
 35 40 45

Arg Ile Arg Gly Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn
 50 55 60

Pro Ser Val Val
 65

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.3 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..50
- (D) OTHER INFORMATION: /note= "putative RAP2.3 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Asn Val Tyr Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15

Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr
 20 25 30

Phe Asn Thr Ala Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys
 35 40 45

Gln Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Asp Leu His His
 50 55 60

Pro Pro Pro Pro
 65

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.5 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix (SEQ ID NO:39)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu	Ile	Arg	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Pro	Trp	Gly	Arg	Tyr	Ala
1					5					10					15
Ala	Glu	Ile	Arg	Asp	Pro	Gly	Lys	Lys	Thr	Arg	Val	Trp	Leu	Gly	Thr
							20		25					30	
Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Thr	Ala	Ala	Arg
							35		40					45	
Asp	Phe	Arg	Gly	Ala	Lys	Ala	Lys	Thr	Asn	Phe	Pro	Thr	Phe	Leu	Glu
							50		55					60	
Leu	Ser	Asp	Gln												
							65								

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.6 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.6 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro	Lys	Lys	Tyr	Arg	Gly	Val	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala
1						5				10					15
Ala	Glu	Ile	Arg	Asp	Pro	His	Lys	Ala	Thr	Arg	Val	Trp	Leu	Gly	Thr
							20		25					30	
Phe	Glu	Thr	Ala	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Leu		
							35		40					45	

Arg	Phe	Arg	Gly	Ser	Lys	Ala	Lys	Leu	Asn	Phe	Pro	Glu	Asn	Val	Gly
50					55					60					
Thr	Gln	Thr	Ile												
65															

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.12 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.12 amphipathic alpha-helix (SEQ ID NO:40)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala
1				5					10				15		

Ala	Glu	Ile	Arg	Asp	Pro	Arg	Glu	Gly	Ala	Arg	Ile	Trp	Leu	Gly	Thr
		20					25						30		

Phe	Lys	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Arg
	35					40						45		

Arg	Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Asn	Met
	50				55				60					

Lys	Ala	Asn	Ser
65			

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis TINY AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative TINY amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

His	Pro	Val	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Asn	Trp	Gly	Lys	Trp	Val
1					5						10				15

Ser	Glu	Ile	Arg	Glu	Pro	Arg	Lys	Lys	Ser	Arg	Ile	Trp	Leu	Gly	Thr
	20						25								30

Phe	Pro	Ser	Pro	Glu	Met	Ala	Ala	Arg	Ala	His	Asp	Val	Ala	Ala	Leu
					35			40							45

Ser	Ile	Lys	Gly	Ala	Ser	Ala	Ile	Leu	Asn	Phe	Pro	Asp	Leu	Ala	Gly
	50					55									60

Ser	Phe	Pro	Arg
	65		

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.1 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg	Lys	Pro	Tyr	Arg	Gly	Ile	Arg	Arg	Arg	Lys	Trp	Gly	Lys	Trp	Val
1					5					10					15

Ala Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser
 20 25 30

Tyr Thr Thr Asp Ile Ala Ala Arg Ala Tyr Asp Val Ala Val Phe
 35 40 45

Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu
 50 55 60

Gln Glu Glu Asp
 65

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Clif

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.4 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.4 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Thr Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly Lys Trp Val
 1 5 10 15

Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp Leu Gly Thr
 20 25 30

Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala Tyr
 35 40 45

Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asn Leu Arg His
 50 55 60

Asn Gly Phe His
 65

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.8 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..48
- (D) OTHER INFORMATION: /note= "putative RAP2.8 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly
 1 5 10 15

Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn
 20 25 30

Glu Gln Glu Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe
 35 40 45

Arg Gly Arg Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly
 50 55 60

Asp Leu
 65

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.10 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..51
- (D) OTHER INFORMATION: /note= "putative RAP2.10 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp	Lys	Pro	Tyr	Lys	Gly	Ile	Arg	Met	Arg	Lys	Trp	Gly	Lys	Trp	Val
1				5					10					15	
Ala	Glu	Ile	Arg	Glu	Pro	Asn	Lys	Arg	Ser	Arg	Ile	Trp	Leu	Gly	Ser
	20						25						30		
Tyr	Ser	Thr	Pro	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Thr	Ala	Val	Phe	
		35					40						45		
Tyr	Leu	Arg	Gly	Pro	Ser	Ala	Arg	Leu	Asn	Phe	Pro	Glu	Leu	Leu	Ala
		50					55					60			
Gly	Val	Thr	Val												
	65														

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.11 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..50
- (D) OTHER INFORMATION: /note= "putative RAP2.11 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Lys	Thr	Lys	Phe	Val	Gly	Val	Arg	Gln	Arg	Pro	Ser	Gly	Lys	Trp	Val
1				5					10					15	
Ala	Glu	Ile	Lys	Asp	Thr	Thr	Gln	Lys	Ile	Arg	Met	Trp	Leu	Gly	Thr
	20						25						30		
Phe	Glu	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Glu	Ala	Ala	Cys
		35						40					45		

Leu Leu Arg Gly Ser Asn Thr Arg Thr Asn Phe Ala Asn His Phe Pro
50 55 60
Asn Asn Ser Gln
65

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Val or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Arg Gly Xaa Arg
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = positively charged
amino acid"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Trp, Phe or Tyr"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Asp or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Trp Gly Xaa Xaa Xaa Ala Glu Ile Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Tyr or Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Trp Leu Gly Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile, Leu or positively charged amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Glu Ala Ala Xaa Ala Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "putative RAP2.7-R1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
1 5 10 15

Phe

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CH Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg
 1 5 10 15
 Ile Arg

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Thr Ala Ala Arg Asp Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.12
amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg
1 5 10 15

Ile Arg

(2) INFORMATION FOR SEQ ID NO:41:

CH
✓

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative EREBP-3
amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Ala Glu Glu Ala Ala Lys Ala Tyr Asp Thr Ala Ala Arg Glu Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "AP2 linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Lys Gln Met Thr Asn Leu Thr Lys Glu Glu Phe Val His Val Leu Arg
1 5 10 15

Arg Gln Ser Thr Gly Phe Pro Arg Gly
20 25

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

C

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "ANT linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Asp Met Met Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu
1 5 10 15

Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly
20 25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "RAP2.7 linker region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Lys	Gln	Val	Gln	Asn	Leu	Ser	Lys	Glu	Glu	Phe	Val	His	Ile	Leu
1				5				10						15	
Arg	Arg	Gln	Ser	Thr	Gly	Phe	Ser	Arg	Gly						
			20				25								

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = positively charged
amino acid"

✓
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asn	Leu	Thr	Xaa	Glu	Glu	Phe	Val	His
1			5					

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu	Arg	Arg	Gln	Ser	Thr	Gly	Phe	Ser	Arg	Gly
1				5				10		

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JOAP2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTGCCGCTG CCGTAGTG

18

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JOAP2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGTCATCCT GAGCCGCATA TC

22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "JORAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTCAAGAAGA AGTGCCTAAC CACG

24

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGAAGCTA GAAGAGCGTC GA

22

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JORAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAATGGG CTGCGGAG

18

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTTACCTCCA GCATCGAACG AG

22

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTGGATCTT GTTCGCTTA CG

22

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTTCAAGCT TAGCGTCGAC TG

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGATGGGCTT GAAACCCGAC

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JORAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTGGCTAGGG CTACGCGC

18

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTCTTTGCCT CCTCAACCAT TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.6L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCTGAGTTCC AACATTTTCG GG

22

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAAATTGGTA ACTCCGGTTC CG

22

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCATTTGCT TTGGCGCATT AC

22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "JORAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCGTTACGC CTCTACCGG

19

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCCGTCTTC CAGAACGTTC

20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "JORAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATCACGGATC TGGCTTGGTT C

21

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "JORAP2.9L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCCTTCTTCC GTATCAACGT CG

22

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..19
 (D) OTHER INFORMATION: /note= "JORAP2.10U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCAACTCCG GCGGTTACG

19

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "JORAP2.10L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTCCTTATA TACGCCGCCG A

21

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "JORAP2.11U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAGAAGAGCA AAGGCAACAA GAC

23

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "JORAP2.11L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGTTGTTAGG AAAATGGTTT GCG

23

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "JORAP2.12U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAACCATTG TTTCACTTC GACTC

25

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "JORAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCACAGAGCG TTTCTGAGAA TTAGC

25

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "AP2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGTGGGATC TAAACGACGC AC

22

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..19
 (C) STRANDEDNESS: single
 (D) OTHER INFORMATION: /note= "AP2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCTTGGTC CACGCCGAC

19

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /note= "RAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AAGAGGACCA TCTCTCAG

18

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AACACTCGCT AGCTTCTC

18

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGGTCAGCA GCCAACAC

18

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAATGCATAG AGCTTGAGG

19

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.4U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ACGGATTTCATCGGAG

18

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.4L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAAGCTAGA ATCGAATCC

19

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TACCGGTTTC GCGCGTAG

18

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:


 (A) NAME/KEY: -
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "RAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CACCTTCGAA ATCAACGACC G

21

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCCCCGAAA ATGTTGGAAC TC

22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "RAP2.6L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TGGGAGAGAA AAAATTGGTA GATCG

25

(2) INFORMATION FOR SEQ ID NO:83:

Cont

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CGATGGAGAC GAAGACTC

18

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTCGGAACCG GAGTTACC

18

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCACTCAAAG GCCGAGATC

19

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TAACAAACATC ACCGGCTCG

19

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCTT AGGAGGAG

18

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

*Cly
Cm*

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.9L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGCCTCATAT GAGTCAGAG

19

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.10U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCCCGGAGCT TTTAGCCG

18

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.10L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAACCCGTTC CAACGATCC

19

(2) INFORMATION FOR SEQ ID NO:91:

UJ

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "RAP2.11U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTCTTCACCA GAAGCAGAGC ATG

23

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.11L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTCCATTGAT TGCATATAGG GACG

24

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.12U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCTTTGGTTC AGAACTCGAA CATC

24

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGGTTGATAA ACGAACGATG CG

22

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Lys Lys Ser Arg
1

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCATGCCAC GATCAACC

18

(2) INFORMATION FOR SEQ ID NO:97:

C I Y U N

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGCAGTCCAA TGCGACGG

18

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Trp Ala Ala Glu Ile Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Ala Asp Ser
1

(2) INFORMATION FOR SEQ ID NO:100:

*C1
Cmt*

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: /note= "RAP2.1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAAGAGTCTA CGATGAGAAA GAGAAGGCAG CCACCTCAAG AAGAAGTGCC TAACCACGTG	60
GCTACAAGGA AGCCGTACAG AGGGATACGG AGGAGGAAAGT GGGGCAAGTG GGTGGCTGAG	120
ATTCGTGAGC CTAACAAACG CTCACGGCTT TGGCTTGGCT CTTACACAAAC CGATATCGCC	180
GCCGCTAGAG CCTACGACGT GGCCGTCTTC TACCTCCGTG GCCCCTCCGC ACGTCTCAAC	240
TTCCCTGATC TTCTCTTGCA AGAAGAGGAC CATCTCTCAG CCGCCACCAC CGCTGACATG	300
CCCGCAGCTC TTATAAGGGA AAAAGCGCG GAGGTGGCG CCAGAGTCGA CGCTCTTCTA	360
GCTTCTGCCG CTCCTTCGAT GGCTCACTCC ACTCCGCCGG TAATAAAACC CGACTTGAAT	420
CAAATACCCG AATCCGGAGA TATATAGTCA ATTTATATAC ATGTAGTTG TTTTGTGTTGA	480
TTAGAAGATT ACATTTACAT ACAAGATACA CATAGATACT GGAAAATATA GGTATGTATA	540
CATTCATAAA TTATCTTATG TATCAAAGAA TTTTATAGAT TCTGATTAGC TTTTTGTTT	600

TGTTTTGAT AAGAACTCTG ATTAGTTGTC CGGAGACAAA ACCGGCTAAG AGCAATCCAT	660
GAGAAGCTAG CGAGTGTGTT TTAGTTCAAG TTGTAATATA AATGCATATT AATTCTTAG	720
TAATTTGT	729

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1101
- (C) OTHER INFORMATION: /note= "RAP2.2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTCCTTGGG GAAAATGGGC TGCAGGAGATC CGTGATCCGA GAAAAGGCTC CCGAGAATGG	60
CTTGGAACAT TCGACACTGC TGAGGAAGCA GCAAGAGCTT ATGATGCTGC AGCACGCAGA	120
ATCCGTGGCA CGAAAGCTAA GGTGAATTT CCCGAGGAGA AGAACCCCTAG CGTCGTATCC	180
CAGAAACGTC CTAGTGCTAA GACTAATAAT CTTCAGAAAT CAGTGGCTAA ACCAAACAAA	240
AGCGTAACCT TGGTTCAGCA GCCAACACAT CTGAGTCAGC AGTACTGCAA CAACTCCTT	300
GACAACCTT TTGGTGATAT GAGTTTCATG GAAGAGAAGC CTCAGATGTA CAACAATCAG	360
TTTGGGTTAA CAAACTCGTT CGATGCTGGA GGTAAACAATG GATACCAGTA TTTCAGTTCC	420
GATCAGGGCA GTAACCCCTT CGACTGTTCT GAGTTGGGT GGAGTGATCA CGGCCCTAAA	480
ACACCCGAGA TCTCTCAAT GCTTGTCAAT AACAAACGAAG CATCATTGAT TGAAGAAACC	540
AATGCAGCCA AGAAGCTCAA ACCAAACTCT GATGAGTCAG ACGATCTGAT GGCATACCTT	600
GACAACGCCT TGTGGGACAC CCCACTAGAA GTGGAAGCCA TGCTTGGCGC AGATGCTGGT	660
GCTGTGACTC AGGAAGAGGA AAACCCAGTG GAGCTATGGA GCTTAGATGAT GATCAATTTC	720
ATGCTGGAAG GAGACTTTG AAGTGATCGA TGGTTCCCTTA GTTTGTAAAT AAAGCTGTGT	780
TGGATTTGC TGTTGGGGGA TGGTACAAGT CACACCTCAA GCTCTATGCA TTGGTATCTC	840
ATGAGCCTTC TCTTCCATAG AGAGTTCTC TTTAATTTT GTCGAAATAA AAAAGGTGTG	900
ATGAAGTAAA TAGAGGTATA ATAATATCTA TCTATTAAGT CTTGTTTGT TCTTCATT	960
TTGTATTTCT TTTCTATTTA AAAGACAGTT TATTAGTCTT CTGAGCTCTC TTTTGATCT	1020
TTGTTATAGC GTATCATCAC CCTCGAAAGT GTAATGTTT GTACCCCCAA ACTTGTAG	1080

CATTATAATA AAGTCTCTTT G

1101

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1055
- (C) *✓*
- (D) OTHER INFORMATION: /note= "RAP2.3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATAAAGGCAT	TTCAGCTCCA	CCGTAGGAAA	CTTTCTCTTG	AAAGAAACCC	ACAGCAACAA	60
ACAGAGAAAA	TGTGTGGCGG	TGCTATTATT	TCCGATTATG	CCCCTCTCGT	CACCAAGGCC	120
AAGGGCCGTA	AACTCACGGC	TGAGGAACTC	TGGTCAGAGC	TCGATGCTTC	CGCCGCCGAC	180
GACTTCTGGG	GTTTCTATTTC	CACCTCCAAA	CTCCATCCCA	CCAACCAAGT	TAACGTGAAA	240
GAGGAGGCAG	TGAAGAAGGA	GCAGGCAACA	GAGCCGGGGA	AACGGAGGAA	GAGGAAGAAT	300
GTTTATAGAG	GGATACGTAACG	GGCTCCATGG	GGAAAATGGG	CGGCTGAGAT	TCGAGATCCA	360
CGAAAAGGTG	TTAGAGTTTG	GCTTGGTACG	TTCAACACGG	CGGAGGAAGC	TGCCATGGCT	420
TATGATGTTG	CGGCCAAGCA	GATCCGTGGT	GATAAAGCCA	AGCTCAACTT	CCCAGATCTG	480
CACCATCCTC	CTCCTCCTAA	TTATACTCCT	CCGCCGTCA	CGCCACGATC	AACCGATCAG	540
CCTCCGGCGA	AGAAGGTCTG	CGTTGTCTCT	CAGAGTGAGA	GCGAGTTAAG	TCAGCCGAGT	600
TTCCCGGTGG	AGTGTATAGG	ATTTGGAAAT	GGGGACGAGT	TTCAGAACCT	GAGTTACGGA	660
TTTGAGCCGG	ATTATGATCT	GAAACAGCAG	ATATCGAGCT	TGGAATCGTT	CCTTGAGCTG	720
GACGGTAACA	CGGCGGAGCA	ACCGAGTCAG	CTTGATGAGT	CCGTTCCGA	GGTGGATATG	780
TGGATGCTTG	ATGATGTCAT	TGCGTCGTAT	GAGTAAAAGA	AAAAAAATAA	GTTTAAAAAA	840
AGTTAAATAA	AGTCTGTAAT	ATATATGTAAC	CCGCCGTTAC	TTTTAAAAGG	TTTTTACCGT	900
CGCATTGGAC	TGCTGATGAT	GTCTGTTGTG	TAATGTGTAG	AATGTGACCA	AATGGACGTT	960
ATATTACGGT	TTGTGGTATT	ATTAGTTCT	TAGATGGAAA	AACTTACATG	TGTAATAAG	1020
ATTTGTAATG	TAAGACGAAG	TACTTATAAC	TTCTT			1055

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

C1 with

- (A) NAME/KEY: -
- (B) LOCATION: 1..969
- (D) OTHER INFORMATION: /note= "RAP2.4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TCTTCCTCCG	ACGCATCACA	ACAACAAACAA	CTCTTCTCG	AATCTTCTCA	GCCCAAAGCC	60
GTACTGATG	AAGCAATCTG	GAGTCGCTGG	ATCTTGTTC	GCTTACGGTT	CAGGTGTTCC	120
TTCGAAGCCG	ACGAAGCTTT	ACAGAGGTGT	GAGGCAACGT	CACTGGGGAA	AATGGGTGGC	180
TGAGATCCGT	TTGCCGAGAA	ATCGGACTCG	TCTCTGGCTT	GGGACTTTG	ACACGGCGGA	240
GGAAGCTGCG	TTGGCCTATG	ATAAGGCGGC	GTACAAGCTG	CGCGGCGATT	TCGCCCCGGCT	300
TAACCTCCCT	AACCTACGTC	ATAACGGATT	TCACATCGGA	GGCGATTCG	GTGAATATAA	360
ACCTCTTCAC	TCCTCAGTCG	ACGCTAAGCT	TGAAGCTATT	TGTAAAAGCA	TGGCGGAGAC	420
TCAGAACAG	GACAAATCGA	CGAAATCATC	GAAGAAACGT	GAGAAGAAGG	TTTCGTCGCC	480
AGATCTATCG	GAGAAAGTGA	AGGCAGGAGGA	GAATTGGTT	TCGATCGGTG	GATCTCCACC	540
GGTACGGAG	TTTGAAGAGT	CCACCGCTGG	ATCTTCGCCG	TTGTCGGACT	TGACGTTCGC	600
TGACCCGGAG	GAGCCGCCGC	AGTGGAACGA	GACGTTCTCG	TTGGAGAAGT	ATCCGTCGTA	660
CGAGATCGAT	TGGGATTCGA	TTCTAGCTTA	GGGGAAAT	AGGAAATTCA	GCCGCTTGCA	720
ATGGAGTTTT	TGTGAAATTG	CATGACTGGC	CCAAGAGTAA	TTAATTAAAT	ATGGATTAGT	780
GTAAATTTC	GTATGTTAAT	ATTTGTATTA	TGGTTGTAT	TAGTCTCTCT	GTGTCGGTCC	840
AGCTTGCAGG	TTTTGTCAG	GCTCGACCAT	GCCACAGTTT	TCATTTATG	TAATCTTTT	900
TTCTTTGTC	TTATGTAATT	TGTAGCTCA	GTTCTTCAT	CTATAATGCA	ATTTTATTAT	960
GATTATGTG						969

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..937
- (C) OTHER INFORMATION: /note= "RAP2.5"

CJ
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GTCGACCCAC GCGTCCGACT CTCTCTCTAA TCTATCTATC CGAGAATGGC CAAGATGGC	60
TTGAAACCCG ACCCGGCTAC TACTAACCAAG ACCCACATAA ATGCCAAGGA GATTGTTAC	120
AGAGGCGTTA GGAAGCGTCC TTGGGGCCGT TATGCCGCCG AGATCCGAGA TCCGGGCAAG	180
AAAACCCGCG TCTGGCTTGG CACTTCGAT ACGGCTGAAG AGGCGGCGCG TGCTTACGAT	240
ACGGCGGCCGC GTGATTTCG TGGTGCTAAG GCTAAGACCA ATTTCCAAC TTTTCTCGAG	300
CTGAGTGACC AGAAGGTCCC TACCGGTTTC GCGCGTAGCC CTAGCCAGAG CAGCACGCC	360
GACTGTGCTT CTCCTCCGAC GTTAGTTGTG CCTTCAGCGA CGGCTGGAA TGTTCCCCCG	420
CAGCTCGAGC TTAGTCTCGG CGGAGGAGGC GGCGGCTCGT GTTATCAGAT CCCGATGTCG	480
CGTCCTGTCT ACTTTTGGA CCTGATGGGG ATCGGTAACG TAGGTCGTGG TCAGCCTCCT	540
CCTGTGACAT CGGCGTTAG ATGCCGGTG GTGCATGTTG CGACGAAGAT GGCTTGTGGT	600
GCCCAAAGCG ACTCTGATTC GTCATCGTC GTTGATTCG AAGGTGGAT GGAGAAGAGA	660
TCTCAGACTG TTAGATCTAG ATCTTAATTT GCCTCCTCCA TCGGAACAGG CCTGAGCTT	720
TAACGGTGTC GTTTCAATTC GAAGCGCATG CGTTTCTTCT TCTTTTGAG CTGTGAAAAT	780
TCGTTTCTC ATAGTTTTC CTCTCTCTCT CTCTCAGTCT AAATTATTA CCAGTTTTA	840
GAAAGAAAAA ACAGATTAAA TCTGAGAGAG AAAATATAA TTTAGCTGA CATGGATCGT	900
TATGTACATA TTATTACATA ACCGGAGATC TGAACGT	937

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..651
- (C) OTHER INFORMATION: /note= "RAP2.6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AAGAGAAGAG	TTTCCTTG	CTCCTCAACC	ATTGATTACC	GGTCAGCTG	TGACTAAAGA	60
ATGTGAAAGC	TCAATGTCCT	TGGAGAGGCC	AAAAAAATAT	AGAGGAGTAA	GGCAACGACC	120
ATGGGGAAAA	TGGCGGCCGG	AGATTCGAGA	CCCACACAAG	GCGACACGTG	TATGGCTTGG	180
GACATTGAG	ACAGCCGAGG	CCGCCGCAAG	AGCCTATGAT	CGGGCAGCAC	TTCGCTTAG	240
AGGAAGCAA	GCAAAGCTTA	ATTCCTCGA	AAATGTTGGA	ACTCAGACGA	TTCAACGAAA	300
TTCTCATTTC	TTGCAAAACT	CAATGCAACC	TTCTCTAAC	TACATCGATC	AATGTCCAAC	360
TCTATTATCT	TACTCTCGAT	GTATGGAGCA	ACAACAACCA	TTAGTAGGCA	TGTTGCAGCC	420
AACAGAAGAG	GAAAATCACT	TTTCGAAAA	ACCATGGACC	GAATATGATC	AATACAATT	480
CTCCTTTT	GGTTAACTAA	CATATCGTCA	ACGCTTGTA	TTTCTACTTA	TTCGATCTAC	540
CAATTTTTC	TCTCCAAATA	CAAATTCAGT	CTGATTATTG	CCTTCTTAGA	TATGTCTTCG	600
AATGTTATGA	CTATACATGG	GTGTATATAA	AATTGTGAT	CAAAGTCTTG	T	651

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

C
WT

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1329
- (D) OTHER INFORMATION: /note= "RAP2.7"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AATGCCGATG	GAGACGAAGA	CTCTTGCTCT	ACTCGAGCTT	TCACTCTCAG	TTTCGATATT	60
TTAAAAGTCG	GAAGTAGTAG	CGGCAGAGAC	GAAAGCCCCG	CCGCTTCAGC	TTCCGTTACT	120
AAAGAGTTTT	TTCCGGTGAG	TGGAGACTGT	GGACATCTAC	GAGATGTTGA	AGGATCATCA	180
AGCTCTAGAA	ACTGGATAGA	TCTTCTTTT	GACCGTATTG	GTGACGGAGA	AACGAAATTG	240
GTAACCTCCGG	TTCCGACTCC	GGCTCCGGTT	CCGGCTCAGG	TTAAAAAGAG	TCGGAGAGGA	300
CCAAGGTCTA	GAAGTTCAC	GTATAGAGGA	GTACTTTTT	ATAGAAGAAC	TGGTCGATGG	360
GAGTCACATA	TTGGGGATTG	TGGGAAACAA	GTATTATTTAG	GTGGTTTCGA	CACTGCTCAT	420
GCTGCAGCTA	GAGCTTATGA	TCGAGCTGCT	ATTAATTTA	GAGGTGTTGA	TGCTGATATC	480
AACTTTACTC	TTGGTGATTA	TGAGGAAGAT	ATGAAACAGG	TACAAAACCT	GAGTAAGGAA	540

GAGTTTGTGC ATATACTGCG TAGACAGAGC ACGGGGTTT CGCGGGGAG TTCGAAGTAT	600
CGAGGGGTTA CGTTACACAA ATGTGGTAGA TGGGAAGCTA GGATGGGCA GTTTCTTGGT	660
AAAAAGGCTT ATGACAAGGC TGCAATCAAC ACTAATGGTA GAGAAGCAGT CACGAACCTC	720
GAGATGAGTT CATAACCAAAA TGAGATTAAC TCTGAGAGCA ATAACCTCTGA GATTGACCTC	780
AACTTGGGAA TCTCTTATC GACCGGTAAT GCGCCAAAGC AAAATGGGAG GCTCTTCAC	840
TTCCCTTCTA ATACTTATGA AACTCAGCGT GGAGTTAGCT TGAGGATAGA TAACGAATAC	900
ATGGGAAAGC CGGTGAATAC ACCTCTTCCT TATGGATCCT CGGATCATCG CCTTTACTGG	960
AACGGAGCAT GCCCGAGTTA TAATAATCCC GCCGAGGGAA GAGCAACAGA AAAGAGAAGT	1020
GAAGCTGAAG GGATGATGAG TAACTGGGAA TGGCAGAGAC CGGGGCAAAC AAGGCCGTG	1080
AGACCGCAGC CACCGGGACC ACAACCACCA CCATTGTTCT CAGTTGCAGC AGCATCATCA	1140
GGATTCTCAC ATTTCCGGCC ACAACCTCCC AATGACAATG CAACACGTGG TTACTTTAT	1200
CCACACCCCTT AACTTGTAAG GGGACATATG AGAGTTTTT TACCATCTCT CTCTCTCTCA	1260
ACACTCTAGT CCCCTTCAA AAATGTCATT TGGGTTTAG ATTTTCACA TACAATGATC	1320
AATTTTTCC	1329

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1113 base pairs

 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..1113
 (D) OTHER INFORMATION: /note= "RAP2.8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCACCACC GCCAAGAAC TCTCTCTCC TCCCGCGGCG GCGTTACGCC TCTACCGGAT	60
GGGAAGCGGC GGGAGCAGCG TCGTGTGGA TCCCGAGAAC GGCCTAGAGA CGGAGTCACG	120
AAAGCTACCA TCTTCAAAAT ACAAAAGGTGT TGTTCTCAG CCTAACGGAA GATGGGGAGC	180
TCAGATCTAC GAGAACGACC AACGAGTATG GCTCGGGACT TTCAACGAGC AAGAAGAAC	240
TGCTCGTTCC TACGACATCG CAGCTTGTAG ATTCCGTGGC CGCGACGCCG TCGTCAACTT	300
CAAGAACGTT CTGGAAGACG GCGATTTAGC TTTTCTTGAA GCTCACTCAA AGGCCGAGAT	360
CGTCGACATG TTGAGAAAAC ACACCTACGC CGACGAGCTT GAACAGAACAA ATAAACGGCA	420

GTTGTTTCTC TCCGTCGACG CTAACGGAAA ACGTAACGGA TCGAGTACTA CTCAAAACGA	480
CAAAGTTTA AAGACGTGTG AAGTTCTTT CGAGAAGGCT GTTACACCTA GCGACGTTGG	540
GAAGCTAAC CGTCTCGTGA TACCTAAACA ACACGCCGAG AAACACTTTC CGTTACCGTC	600
ACCGTCACCG GCAGTGACTA AAGGAGTTT GATCAACTTC GAAGACGTTA ACGGTAAAGT	660
GTGGAGGTTG CGTTACTCAT ACTGGAACAG TAGTCAAAGT TACGTGTTGA CCAAGGGATG	720
GAGTCGATTG GTCAAGGAGA AGAATCTCG AGCCGGTGAT GTTGTACTT TCGAGAGATC	780
GACCGGACTA GAGCGGCAGT TATATATTGA TTGGAAAGTT CGGTCTGGTC CGAGAGAAAA	840
CCCGGTTCAAG GTGGTGGTTC GGCTTTCCGG AGTTGATATC TTTAATGTGA CCACCGTGAA	900
GCCAAACGAC GTCGTGGCCG TTTGCGGTGG AAAGAGATCT CGAGATGTTG ATGATATGTT	960
TGCGTTACGG TGTTCCAAGA AGCAGGCGAT AATCAATGCT TTGTGACATA TTTCCCTTTTC	1020
CGATTTATG CTTTCGTTT TTAATTTTT TTTTGTCAA GTTGTGAGG TTGTGATTCA	1080
TGCTAGGTTG TATTTAGGAA AAGAGATAAG ACC	1113

(2) INFORMATION FOR SEQ ID NO:108:

C/Int

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..417
 - (D) OTHER INFORMATION: /note= "RAP2.9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CGATCACCGA TCTGGCTTGG TTCATACAAA ACCGCCGTTG CCGCGGCACG GGCCTACGAT	60
ACCGCTGTGT TTTACTTACG TGGTCCTTCG GCGAGACTCA ATTTCCCTGA AGAGGTCTTT	120
AAGGATGGAA ACGGCGGTGA AGGCTTAGGA GGAGATATGT CTCCGACGTT GATACTGGAAAG	180
AAGGCGGCTG AGGTGGGAGC TAGAGTCGAC GCAGAGTTGC GGTTAGAGAA TAGGATGGTT	240
GAGAACTTAG ACATGAATAA GTTGCCGGAG GCATATGGAT TGTAATTAT AGTTGGTAG	300
TTTATAGGTT GGAGATTGCC CGGAGACAGA GTCAAACAGA GGTTCTCTGA CTCATATGAG	360
GCATAATATA GTTAATATAG TAATTTTGT TTTGAGCATA GTAATTATGT CATAACC	417

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..814
- (C) OTHER INFORMATION: /note= "RAP2.10"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATTTTTTGAA	ACTTCTTCTC	TTTGCGGTT	TCGTGTTCCA	CTCCTCTCTT	CTTGGCCCAC	60
GTGTTCATCA	ATCTCTCCCT	CCGCATGTAA	TCGCTTCGCC	GTCAATATCA	CATCTTCTT	120
CTTCTTTATC	TTTAAAATCT	CTTTAGATCG	ATTCTTTGT	GGATTCTTGA	AATCTCCGGA	180
GAAAACCACT	ATGGAGACGG	CGACTGAAGT	GGCCACGGTG	GTGTCAACTC	CGGCGGTTAC	240
GGTTGCGGCG	GTGGCGACGA	GGAAGAGAGA	TAAGCCGTAT	AAAGGGATAA	GGATGAGGAA	300
GTGGGGGAAG	TGGGTGGCGG	AGATAAGAGA	GCCTAATAAA	AGGTCAAGGA	TCTGGCTTGG	360
CTCTTACTCT	ACTCCTGAAG	CGGCGGCGCG	TGCTTACGAC	ACGGCGGTGT	TTTATCTCCG	420
AGGTCCCTCT	GCTCGGCTTA	ACTTCCCGGA	GCTTTAGCC	GGAGTGACGG	TGACGGGAGG	480
AGGCGGAGGA	GGAGTGAAACG	GTGGTGGAGA	TATGTCGGCG	GCGTATATAA	GGAGAAAAGC	540
GGCGGAGGTT	GGAGCACAAG	TGGATGCGTT	AGAAGCGGCG	GGGGCGGGAG	GGAATCGTCA	600
TCATCATCAT	CATCAACATC	AACGTGGTAA	TCATGATTAC	GTAGATAATC	ATAGTGATTAA	660
TCGTATTAAT	GATGATCTTA	TGGAGTGTAG	TAGTAAAGAA	GGGTTTAAGA	GGTGTAAATGG	720
ATCGTTGGAA	CGGGTTGATT	TAAACAAATT	ACCCGATCCG	GAAACTTCAG	ATGACGATTA	780
GGAAAGCAAA	AAATAGAAAC	AAAAAAAAAA	AAAA			814

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..933
- (D) OTHER INFORMATION: /note= "RAP2.11"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AAAAAAATAT GGAACATCAA ACAACTCAA AGCAGAAAAC TAAGGAGAAG AGCAAAGGCA	60
ACAAGACTAA ^{5'} GTTTGTGGGA GTTAGGCAAA GGCCTTCAGG AAAATGGGTG GCAGAGATCA	120
AAGACACTAC ACAAAAGATA CGGATGTGGC TCGGAACCTT TGAAACCGCA GAAGAAGCCG	180
CTCGAGCCTA CGATGAAGCT GCATGTCTCT TACGTGGCTC CAATACTCGC ACCAATTCG	240
CAAACCATT TCCTAACAAAC TCACAACAT CTTTGAAGAT CAGAAATCTT CTTCACCAGA	300
AGCAGAGCAT GAAGCAGCAG CAACAACAAAC AACACAAACC AGTTTCTTCT TTAACGGATT	360
GCAACATCAA CTACATCTCG ACTGCTACTA GTCTCACCAC AACCACCACC ACCACCACTA	420
CCACGGCCAT ACCGCTCAAT AATGTGTACC GACCAGATTG ATCGGTCTT GGGCAACCAG	480
AAACCGAGGG TCTCCAGCTT CCTTATTCTG GGCCCCTTGT CTCTGGATTG AACCATCAGA	540
TTCCATTGGC TCAGGCAGGG GGAGAAACAC ATGGACATCT CAACGATCAC TACTCAACCG	600
ATCAACATTG GGGTCTTGCA GAAATTGAAA GACAGATATC TGCGTCCCTA TATGCAATGA	660
ATGGAGCTAA CAGTTACTAT GACAACATGA ATGCAGAATA TGCAATTTC GATCCTACCG	720
ATCCCATTG GGATCTCCCT TCACTCTCCC AACTCTTCTG CCCTACGTGA TTTCCAATTG	780
ACTTTCTG ATCAATTCTAT GTAATGTTTG GATCAATGAT CCATGATTGT AAAGTAGAAC	840
ACATCTCTAC AATGTTCCAA TAGACAAGAT TGTACCTAAA GAAAATGGAC AATGTAAGAA	900
GATAATGAAG GTTTCGTACA ACAAAAGCTT GAT	933

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1277
- (D) OTHER INFORMATION: /note= "RAP2.12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CGTTCGAATT TCTTCGATT TGACGCTGAG TTCGAAGCTG ATTTCCAAGG TTTCAAAGAT	60
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GATTCGTCTA TCGATTGCGA TGATGATTTC GACGTCGGTG ATGTTTCGC CGATGTGAAA	120
CCATTCGTTT TCACCTCGAC TCCAAAACCC GCCGTCTCCG CCGCTGCGGA AGGTCAGTT	180
TTTGGTAAGA AAGTTACTGG CTTGGATGGG GACGCTGAGA AATCTGCAAA TAGGAAGAGG	240
AAGAATCAGT ACCGAGGGAT TAGGCAACGT CCTTGGGGAA AATGGGCTGC TGAGATACGT	300
GATCCAAGGG AAGGTGCTAG AATCTGGCTT GGAACGTTCA AGACAGCTGA GGAAGCTGCT	360
AGAGCTTACG ATGCTGCAGC GCGGAGAATC CGTGGATCTA AAGCTAAGGT GAATTCCTT	420
GAAGAAAACA TGAAGGCTAA TTCTCAGAAA CGCTCTGTGA AGGCTAATCT TCAGAAACCA	480
GTGGCTAAC CTAACCCTAA CCCAAGTCCA GCTTGGTTC AGAACTCGAA CATCTCCTT	540
GAAAATATGT GTTTCATGGA GGAGAACAC CAAGTGAGCA ACAACAACAA CAACCAGTT	600
GGGATGACAA ACTCCGTTGA TGCTGGATGT AATGGGTATC AGTATTTCAG CTCTGACCAG	660
GGTAGTAATT CTTTCGATTG TTGGAGTTT GGTTGGAGCG ATCAAGCTCC GATAACTCCC	720
GACATCTCTT CTGCGGTTAT CAACAACAAC AACTCAGCTC TGTTCTTGA GGAAGCCAAT	780
CCAGCTAAGA AGCTCAAGTC TATGGATTTC GAGACACCTT ACAACAACAC TGAATGGGAC	840
GCTTCACTGG ATTTCCTCAA CGAAGATGCT GTAACGACTC AGGACAATGG TGCAAACCC	900
ATGGACCTAT GGAGTATTGA TGAAATTCAT TCCATGATTG GAGGAGTCTT CTGAAGAGAT	960
CCAGTTTCAT GTAAATAAGG CTGCATGTTT GTGAGTTCC CGCATCGTTC GTTTATCAAC	1020
CTCCAAAACT TTCTAATGTC TGTTACTTGC ATCTTCTTCT GCTGTCTCTG TCTGTCTCTC	1080
TCAGGAGTTC CTGTTGCAT TCGAGAACGC CATGAGCCTC TATCTGAGG GTAGTTGTGA	1140
TGAAGTTAAG TAGAGGCTTA TTTTAGGGG TTGTGGTAGT TTTTGTTTA GTGAATCTT	1200
TGAATTGTT TGTGTTTGT TTTGTTACT TTATGCCCA AAACCTCTT AACATTTGTC	1260
ATAATGTGTT TGAACCT	1277

C
✓
✓